

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2001, 18:08:46 ; Search time 1088.91 Seconds
(without alignments)
12188.502 Million cell updates/sec

Title: US-09-481-990-1
Perfect score: 1894
Sequence: 1 GGGCAGGAGAGACGCGCTGC.....ATATATAAAAAAAAAAAAA 1894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estda:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estov1:*
68: em_estov2:*
69: em_estpl1:*
70: em_estpl2:*
71: em_estpl3:*
72: em_estpl4:*
73: em_estpl5:*
74: em_estro1:*
75: em_estro2:*
76: em_estro3:*
77: em_estro4:*
78: em_estro5:*
79: em_estro6:*
80: em_estro7:*
81: em_estro8:*
82: em_estro9:*
83: em_estro10:*
84: em_estro11:*
85: em_estro12:*
86: em_estro13:*
87: gb_esta1:*
88: gb_esta2:*
89: gb_esta3:*
90: gb_esta4:*
91: gb_esta5:*
92: gb_esta6:*
93: gb_esta7:*
94: gb_esta8:*
95: gb_esta9:*
96: gb_est50:*
97: gb_est51:*
98: gb_est52:*
99: gb_est53:*
100: gb_est54:*
101: gb_est55:*
102: gb_est56:*
103: gb_est57:*
104: gb_est57:*
105: gb_est58:*
106: gb_est59:*
107: gb_est60:*
108: gb_est71:*
109: gb_est72:*
110: gb_est73:*
111: gb_est74:*
112: em_esthum21:*
113: em_esthum22:*
114: em_esthum23:*
115: em_estom1:*
116: em_estom2:*

117: em_estp16:*
 118: em_estp17:*
 119: em_estp18:*
 120: em_estp19:*
 121: em_estp20:*
 122: em_estp21:*
 123: em_estp22:*
 124: em_estp23:*
 125: em_estp24:*
 126: em_estp25:*
 127: em_estp26:*
 128: em_estp27:*
 129: em_estp28:*
 130: em_estp29:*
 131: em_estp30:*
 132: em_estp31:*
 133: em_estp32:*
 134: em_estp33:*
 135: em_estp34:*
 136: em_estp35:*
 137: em_estp36:*
 138: em_estp37:*
 139: em_estp38:*
 140: em_estp39:*
 141: em_estp40:*
 142: em_estp41:*
 143: em_estp42:*
 144: em_estp43:*
 145: em_estp44:*
 146: em_estp45:*
 147: em_estp46:*
 148: em_estp47:*
 149: em_estp48:*
 150: em_estp49:*
 151: em_estp50:*
 152: em_estp51:*
 153: em_estp52:*
 154: em_estp53:*
 155: em_estp54:*
 156: em_estp55:*
 157: em_estp56:*
 158: em_estp57:*
 159: em_estp58:*
 160: em_estp59:*
 161: em_estp60:*
 162: em_estp61:*
 163: em_estp62:*
 164: em_estp63:*
 165: em_estp64:*
 166: em_estp65:*
 167: em_estp66:*
 168: em_estp67:*
 169: em_estp68:*
 170: em_estp69:*
 171: em_estp70:*
 172: em_estp71:*
 173: em_estp72:*
 174: em_estp73:*
 175: em_estp74:*
 176: em_estp75:*
 177: em_estp76:*
 178: em_estp77:*
 179: em_estp78:*
 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	532.4	29.2	676	27	A1956397	A1956397 u174g06.y
2	538.4	28.4	676	27	A1956401	A1956401 u174g11.y
3	535.2	28.3	682	27	A1956216	A1956216 u174g10.y
4	531.6	28.1	586	1	AA001030	AA001030 ze46c10.r
5	518	27.3	626	139	BF030864	BF030864 601557647
6	497.6	26.3	681	107	BE377443	BE377443 601228920
7	492.8	26.0	588	143	N78391	N78391 yz75e05.r1
8	488	25.8	607	37	AV612885	AV612885 AV612885
9	477	25.2	602	13	AA872079	AA872079 o13a07.s
10	474	25.0	475	27	A1934807	A1934807 wp88f11.x
11	454.2	24.0	484	26	A1924793	A1924793 w023a04.x
12	439.4	23.2	551	38	AW012076	AW012076 um07e02.y
13	419	22.1	742	106	BE309179	BE309179 601095044
14	417.2	22.0	434	12	AA858126	AA858126 of65h07.s
15	414.4	21.9	424	1	AA021294	AA021294 ze68g04.r
16	391.2	20.7	481	143	N51100	N51100 yz03e08.s1
17	391	20.6	528	2	AA143352	AA143352 z066d11.s
18	385.8	20.4	471	145	T74333	T74333 yc84f03.r1
19	385	20.3	385	7	AA408660	AA408660 ne06c01.s
20	381.2	20.1	456	16	A1129709	A1129709 qc35h10.x
21	376.2	19.9	518	111	BE720244	BE720244 RC0-HT088
22	373	19.7	381	22	A1566688	A1566688 to21b01.x
23	372	19.6	421	95	AW784337	AW784337 zb61d11.9
24	369.8	19.5	496	87	AW227291	AW227291 um69g11.y
25	369.4	19.5	412	106	BE284810	BE284810 601091118
26	361.8	19.1	417	134	BE088384	BE088384 CM0-EP068
27	359.6	19.0	563	24	A1770078	A1770078 w179g03.x
28	357.8	18.9	401	90	AW429512	AW429512 67771 MAR
29	352.6	18.6	417	21	A1493368	A1493368 t070g12.x
30	352.4	18.6	369	5	AA308453	AA308453 EST179278
31	333	17.6	343	5	AA307980	AA307980 EST179278
32	324.2	17.1	333	4	AA257164	AA257164 z182b09.r
33	319	16.8	539	38	AW012792	AW012792 u187g10.y
34	315.8	16.7	600	107	BE373364	BE373364 601225025
35	314	16.6	536	146	T89472	T89472 ye04g04.s1
36	312.4	16.5	315	147	Z39663	Z39663 HSC1GA022.n
37	307.4	16.2	364	146	T89039	T89039 yc84f03.s1
38	306.2	16.2	418	93	AW619432	AW619432 7488 MARC
39	298	15.7	537	20	A1425785	A1425785 me87e01.y
40	295	15.6	318	147	Z43599	Z43599 HSC1GA021.n
41	281.8	14.9	298	140	F12504	F12504 HSC3AH031.n
42	280.2	14.8	353	142	N46450	N46450 y776g11.s1
43	279.4	14.8	285	140	F03207	F03207 HSC1EP112.n
44	279.4	14.8	604	139	BF046131	BF046131 BP250004A
45	277.2	14.6	323	39	AW020278	AW020278 df07d03.y

ALIGNMENTS

RESULT 1
 A1956397
 LOCUS A1956397 676 bp mRNA
 DEFINITION u174g06.y1 Sugano mouse kidney mRna Mus musculus cDNA clone
 IMAGE:2136346 5' similar to TR:000180 000180 POTASSIUM CHANNEL
 KCNO1. ; mRNA sequence.
 ACCESSION A1956397
 VERSION A1956397.1 GI:5749106
 KEYWORDS EST

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 676)
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Page,D., Hartevey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1001022 Possible reversed clone; similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 466. Location/Qualifiers 1..676
FEATURES	
SOURCE	

			/organism="Mus musculus"		
			/strain="C57BL"		
			/db.xref="taxon:10090"		
			/clone="IMAGE:2136346"		
			/clone_1lb="Sugano mouse kidney mklia"		
			/sex="female"		
			/dev_stage="adult"		
			/lab_host="DHI08"		
			/note="Organ: kidney; Vector: pME18S-FL3; Site:1: DraIII		
			(CACTGATGG); Site:2: DraIII (CACCAATGGG); 1st strand cDNA		
			was primed with an oligo(dT) primer		
			[ATGTGGCTTTTTTTTTTTTTT]		
			ligated to a DraIII adaptor [TGTGGGCTACTGG], digested		
			and cloned into distinct DraIII sites of the pME18S-FL3		
			vector (5' site CACGTGTGG, 3' site CACCAATGG). XhoI should		
			be used to isolate the cDNA insert. Size selection was		
			performed to exclude fragments <1.5kb. Library		
			constructed by Dr. Sumio Sugano (University of Tokyo		
			Institute of Medical Science). Custom primers for		
			sequencing: 5' end primer CTTCGTGCCTTAAGACCTGGC and 3' end		
			primer CGACCTCGACCTCAGCACA."		
BASE COUNT	107 a	210 c	184 g	173 t	2 others
ALIGN					
Query Match		29.2%	Score 552.4;	DB 27;	Length 676;
Best Local Similarity		88.5%;	Pred. No. 2.3e-111;		
Matches 598;	Conservative	0;	Mismatches 78;	Indels	0;
Gaps					
Dn	263 GCTGGGCTAATTGCCTCACTACCTGCTTGTTGGCCCATAGTGCCTTCCTCGTAGGACTGCC	322			
	1 GCTGGGCTAACCTTTTCTCACTGCTGTTGGGCCCTCGTGCCTTCCTCGTAGGACTGCC	60			
Dy	323 CTATGAGGACCTGCTGCGCCAGAGACTCGCAGCACTGAAGCTACACCTTCTTGGAGAGACA	382			
	61 TTATGAGGACCTGCTGCGCCAGAGACTCGCAGCACTGAAGCTACACCTTCTTGGAGAGACA	120			
Dz	383 CGAGTGCCTGCTGTAGACGACACACTGGAGACAGTTCCTGGGCCCTGAGTCTGAGAGCCAGCAA	442			
	121 CGAGTGCCTGCTGTAGAGCCGACACTGGAGACAGTTCCTGGGCCCTGAGTCTGAGAGCCAGCAA	180			
Dx	443 CTACGCGCTGTGCTGCTCAGCAAGAGCCCTCGGGCAACTGAACTGGAGACTTACCCTCCGC	502			
Dy	181 TTATGAGAGTGTGCTGCTCAGCAAGAGCCCTCGGGAAATTTGGAATTTGGAGACTTACCCTCCGC	240			
Dz	503 GCTCTTCTTCCGACACCGTGTCTTCCACACAGAGTTATGTCACACACCGTGTCTTCTTCTT	562			

Db	241	GCTCTTCGTCCAGCAGCGTGCTCTCCACACAGGCAATGGGCACACAGGCCCTGTCTC	300
Oy	622	AGATGAGAGTAAGGCCCTTCTGCAATCATCTACTCCGTCATGGCAATCCCTTACCCTCTCT	622
Db	301	AGATGAGAGGAGAAACCCCTTCTGCAATCATCTACTCTGTCATCGGCAATCCGTTACCCCTCTCT	360
Oy	623	GTTCCTGACGGCTGTGGTCCAGGCGAATCACCGGACAGTCACCGGACGGGCTCTCTA	682
Db	361	CTTCCTGACGGCGGTGGTCCAGGCTGTCACCGGCAATGTCACCGGACCGGACAGTCCTCTA	420
Oy	683	CTTCACATCCGCGTGGGGCTTCTCCAGAAGAGTGTGGCCATCTGCATMGCCGTCTCTCT	742
Db	421	CTTCACATCAATGCGTGGGGCTTCTCCAGAAGAGTGTGGCCATCTGCATMGCCGTCTCTCT	480
Oy	743	TGGGTTGTCTACGTGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGA	802
Db	481	GAGATTGTCTACCGCTTCTGA	540
Oy	803	GGATGATCGGAACCTTCTCTGGAATCTTATAATTTTTTTTATTTTCCGAGACCATTTGG	862
Db	541	GGATGATCGGAACCTTCTCTGGAATCTTATAATTTTTTTTATTTTCCGAGACCATTTGG	600
Oy	863	CCTGGGGATTAATTTGCTGGGAGAGCTACATCAATCAAATTCAGAGACTTATATGAT	922
Db	601	CCTGGGGATTAATTTGCTGGGAGAGCTACATCAATCAAATTCAGAGACTTATATGAT	660
Oy	923	TGGGATCAGCTGTATTC	938
Db	661	CGTATCATCGGTATTC	676
RESULT	2		
A1956401			
LOCUS	A1956401	676 bp	mRNA
DEFINITION	U174911.X1 Sugen mouse kidney mRna Mus musculus cdna clone IMAGE:2136356.5 similar to TR-000180 000180 POTASSIUM CHANNEL KCNQ1.; mRNA sequence.	EST	20-AUG-1999
ACCESSION	A1956401		
VERSION	A1956401.1	GI:5749110	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
AUTHORS	1 (bases 1 to 676) Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pearson,B., Swaller,T., Gibbons,M., Pepe,D., Harvey,N., Schurr,R., Ritten,'E.', Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson.R. The WashU-NCI Mouse EST Project 1999 Unpublished (1999)		
TITLE	Contact: Marra M/WashU-NCI Mouse EST Project 1999		
JOURNAL	Washington University School of Medicine		
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:1001032 Possible reversed clone: similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 519. Location/Qualifiers 1..676 /organism="Mus musculus" /strain="C57BL" /db_xref="taxon:10090" /clone="IMAGE:2136356" /clone_lib="Sugen mouse kidney mRna" /sex="female" /dev_stage="adult"		
FEATURES			
SOURCE			

QY	398	GCACAGCTGGAGCAGTTCCTGGGCGCGAGTCTGGAGCCAGTAACATACGCGGTGGGT	457
Db	277	GCCGCACTGGAGCAGTTCCTGGGCGCGGTCTGGAGCCAGTAATATAGAGTGGGT	336
QY	458	GCTCAGCAACGCTTCGGGCAACTGGAACTGGACTCAGCTCAGCTCTCTTCGGCCAG	517
Db	337	GCTCAGCAACGCTTCGGGAAATGGAAATGGAGCTTCACTCAGCTCAGCTCTTCGGCCAG	396
QY	518	CACCGTGTCTCCACACACAGGTTATGGCCACACCGTCCCTTATCAGATGGAGTAAAGC	577
Db	397	CACCGTGTCTCCACACACAGGCTATGGCCACACCGTCCCTTATCAGATGGAGCAAGC	456
QY	578	CTTCGCACTCATCTACACCGGCACTGGCATATCCCTTCACTCCTGTCTGACGGCTGT	637
Db	457	CTTCGCACTCATCTACCTGTGCATCGGCACTCCGTTCACTCCTGTGAGGGCCGT	516
QY	638	GATCCAGCGCATCAACCGTGACGTCACCGCAGCGCCGCTCTACTTCCACATCCGCTG	697
Db	517	GATCCAGCGGTCAACCGTGATGTCACCGGAGACGATCCTTACTTCCACATFANGCT	576
QY	698	GGGCTTCTCCACAGAGGTGGTGGCCATGTCATGCGGTCTCTTGGGTTTGTACTGT	757
Db	577	GGGCTTCTCCACAGAGGTGGTGGCCATGTCATGCGGTCTCTGTGGATTTGTACCGG	636
QY	758	GTCGCGCTTCTTCATCCCGGCGGCTGTCTGTCTGACTGGAG	803
Db	637	TTCCTGCTTCTTTCATCCCGAGCCCGGTGTCTGTGTCTGGAG	682

[illegible]

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES

```

/organism="Homo sapiens"
/db.xref="GDB:1278737"
/db.xref="RAXON:9606"
/clone="IMAGE:362034"
/clone_lib="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ eye: Vector: pT7Tb (Pharmacia) with a
modified polylinker. Site_1: Not I; Site_2: Eco RI; Site_3:

```

strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCACTGAACTGGAGCGCGCCGCTTTT TTTT TTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D., Ph.D. from the University of Toronto. Libraries constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match	28.1%	Score 531.6	DB 1	Length 586
Best Local Similarity	98.3%	Pred. No. 8.7e-107		
Matches	568	Conservative	0	Mismatches 6; Indels 4; Gaps
QY	583	GCATCATCTACTCCGCTCATTTGGCATTTCCCTTCACCCCTCTGTTCCCTGACGGCTGTGTC	642	
Db	1	GCATCATCTACTCCGCTCATTTGGCATTTCCCTTCACCCCTCTGTTCCCTGACGGCTGTGTC	60	
QY	643	AGCGCATACCGTGCAGCTCACCCGCAAGCGGCTCTTACTTCCACATCCGTGGGCT	702	
Db	61	AGCGCATACCGTGCAGCTCACCCGCAAGCGGCTCTTACTTCCACATCCGTGGGCT	119	
QY	703	TCTCCAACGAGTGGTGCCATGTCGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTC	762	
Db	120	TCTCCAACGAGTGGTGCCATGTCGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTC	179	
QY	763	GCTTCTTCTTCATCCCGGCGCTGTCTTCTCATGTCGAGAGATGACTGNAATCTCTGG	822	
Db	180	GCTTCTTCTTCATCCCGGCGCTGTCTTCTCATGTCGAGAGATGACTGNAATCTCTGG	239	
QY	823	AATCCTTTATTTTGTGTTTATTTTCCCTGACACCATTTGGCTTGGGGATTATGCTCTG	882	
Db	240	AATCCTTTATTTTGTGTTTATTTTCCCTGACACCATTTGGCTTGGGGATTATGCTCTG	299	
QY	883	GGGAAGGCTACAAATCAAAATTCAGAGAGCTTAAGATTGGGATACGTTACCTGC	942	
Db	300	GGGAAGGCTACAAATCAAAATTCAGAGAGCTTAAGATTGGGATACGTTACCTGC	359	
QY	943	TACTTGGCCTTATTTGCCATGTTTGGTAGTTCGGAACCTTCTGTGAATCCTCATGAGCTGA	1002	
Db	360	TACTTGGCCTTATTTGCCATGTTTGGTAGTTCGGAACCTTCTGTGAATCCTCATGAGCTGA	419	
QY	1003	AAAAATTCAGAAAATGTTCTATGTGAAGAAAGACAAAGAGAGAGATC-AGTGCACATC	1061	
Db	420	AAAAATTCAGAAAATGTTCTATGTGAAGAAAGAGACAAAGAGATCAGGTGCACATC	479	
QY	1062	ATAGAGATGACCAACCTGCTCTCTCCGATGCACACACAGGAGCTGGAT--GAAG	1119	
Db	480	ATAGAGATGACCAACCTGCTCTCTCCGATGCACACACAGGAGCTGGATGAAG	539	
QY	1120	AGGACAGAGCAAAATGAGCTTTTGTGGCCACCCAG	1157	
Db	540	AGGACAGAGCAAAATGAGCTTTTGTGGCCACCCAG	577	
RESULT	5			
LOCUS	BF030864	626 bp	mRNA	EST
DEFINITION	601557647E1 NIH_MGC_58	Homo sapiens	cdNA clone IMAGE:3827531	5'
ACCESSION	BF030864			
VERSION	BF030864.1	GI:10738576		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 626)			
	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.			


```

||||| 130 CTACCTGGTGTGGGCGCGGTCTCTCTCGTCCGAGAGTGCCTATGAGAGACTGCT 189
OY 338 GCGCCAGAGAGCTGCGGACAGCTTAAGCGAGCGCTTTTGAGAGACAGAGAGCTGCTGCA 397
Db 190 GCGCAGAGAGCTGCGGACAGCTTAAGCGAGCGCTTTTGAGAGAGAGAGAGAGCTGCTGCA 249
OY 398 GCGAGAGAGAGCTGCGGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 457
Db 250 GCGCAGAGAGAGCTGCGGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309
OY 458 GCTCAGAGAGAGCTGCGGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 517
Db 310 GCTCAGAGAGAGCTGCGGAGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369
OY 518 CACCGTCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 577
Db 370 CACCGTCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 429
OY 578 CTTTCAGATCATCTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 637
Db 430 CTTTCAGATCATCTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489
OY 638 GGTCCAGAGAGATCATCTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
Db 490 GGTCCAGAGAGATCATCTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
OY 698 GGTCTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 757
Db 549 GGTCTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
OY 758 GTCCTCTCTCTCTCATCC 777
Db 609 CTGCTTCTCTCTCATCC 628

```

```

RESULT 7
LOCUS N78391 588 bp mRNA EST 02-APR-1996
DEFINITION yz75e05.r1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA
ACCESSION N78391
VERSION N78391.1 GI:1241092
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maita, M., Parsons, J.,
Ridkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The Mashu-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: reverse ET
High quality sequence stop: 394.
Location/Qualifiers
1..588
/organism="Homo sapiens"
/db_xref="GDB:3904735"
/db_xref="taxon:9606"
/clone="IMAGE:288896"
/clone_1id="Soares_multiple_sclerosis_2NBHMS"
/sex="male"

```

```

/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/Note="Vector: p773d (Pharmacia) with a modified
polylinker V-type; phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTATACCATCTGAAGTGGAGCGGCCGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a cot - 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."
BASE COUNT 136 a 134 c 154 g 160 t 4 others
ORIGIN

```

```

Query Match 26.0%; Score 492.8; DB 143; Length 588;
Best Local Similarity 96.4%; Pred. No. 3e-98;
Matches 536; Conservative 0; Mismatches 14; Indels 6; Gaps 3;

OY 685 TCCACATCCGCTGGGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 744
Db 3 TCCACATCCGCTGGGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62
OY 745 GGTTCACACTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 804
Db 63 GGTTCACACTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 122
OY 805 ATGACTGGAATCTCTCGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 864
Db 123 ATGACTGGAATCTCTCGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 182
OY 865 TGGGGATATATGCTGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 924
Db 183 TGGGGATATATGCTGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 242
OY 925 G----GATCAGCTGTACCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
Db 243 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
OY 981 TTTCTGTAATCTCATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Db 303 TTTCTGTAATCTCATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362
OY 1041 GACGAGATCAGAGTGCATCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1099
Db 363 GACGAGATCAGAGTGCATCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
OY 1100 CCAGCAGCT-GGCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
Db 423 CCAGCAGCTGAGGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
OY 1159 CATCTGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
Db 483 CATCTGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
OY 1219 GAGCAGCAGAGGTCAGG 1234
Db 543 AAGCAGCAGGTCAGG 558

```

```

RESULT 8
LOCUS AV612885 607 bp mRNA EST 30-AUG-2000
DEFINITION AV612885 Bos taurus lung fetus Bos taurus cDNA clone E110048D11 5',
ACCESSION AV612885
VERSION AV612885.1 GI:9748555
KEYWORDS EST.

```

SOURCE
ORGANISM Bos taurus
COW.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 607)
Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
Suzuki, H.
TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Oakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1. 607
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bos taurus lung fetus"
/tissue_type="lung"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pZLI; Site: 1; SalI; Site: 2; NotI; Poly A
was deleted from a NotI site"
BASE COUNT 118 a 184 c 148 g 157 t
ORIGIN

Query Match 25.8%; Score 488; DB 37; Length 607;
Best Local Similarity 89.8%; Pred. No. 3.5e-97;
Matches 53; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

468 GCGTCGGGCACTGGAAGTGGAGTTCACCTCCGCTCTCTCTTCCGACAGACCGTCTC 527
|||||
12 GCGTCGGGGAAGTGGAGTTCACCTCCGCTCTCTCTTCCGACAGACCGTCTC 71
|||||
528 TCACCCAGAGTTATGGCCACACCGCTGCTGTCAATGAGAGGCTTCTGCATC 587
|||||
72 TCCACCCAGAGTTATGGCCACACCGCTGCTGTCAATGAGAGGCTTCTGCATC 131
|||||
588 ATGACACCGCATTTGGCATTCCTCACCCTCTGTTCCGAGAGGGCTGATCCAGCGC 647
|||||
132 ATCTATTCGGTACGACATCTTTCACCTCTGTCTTCGACGACATGCTCCAGCGT 191
|||||
648 ATCACCCTGACGTCACCGGAGCGGCTCTCTACTTCCACATCCGCTGGGCTCTCC 707
|||||
192 GTTACCATCATGTCACCGGAGCGCTCCTTACTTCCACGTCGCTGGGCTTCTCC 251
|||||
708 AAGCAGGTGGTGGCATTCGATCCGCTGCTCTGTTGGTTTGCATGTCCTGCTTC 767
|||||
252 AAGCAGGCAATGGGCAATGTCACGCGGCTCTCTCGTGGTGGTGCACGTCCTTC 311
|||||
768 TTTCTTATCCCGGCGGCTGCTCTCTCAGTCTGGAGATGACGGAACCTCCGGAATCC 827
|||||
312 TTTCTTATCCCGGCGGCTGCTCTCTCAGTCTGGAGATGACGGAACCTCCGGAATCC 371
|||||
828 TTTTATTTTGTATTTCTTCTCTGAGACATTTGGCTGGGAGTTATGTCCTGGGAA 887
|||||
372 TTTTATTTTGTATTTCTTCTCTGAGACATTTGGCTGGGAGTTATGTCCTGGGAG 431
|||||
888 GGTCTACATCAAAAATTCAGAGAGCTTATAGATTGGATGACGTTTACCTGACTT 947
|||||
432 GGTCTACATCAAAAATTCAGAGAGCTTATAGATTGGATGACGTTTACCTGACTT 491
|||||
948 GGCCTTTTGGCATGTTAGTCTGGAACCTTGTGAATCCATGAGCTTAATAAAA 1007
|||||
492 GGTCTCATTCGAATGTTGGTGTCTGGAACCTTGTGTGAGTCCAGAACTGAAGAAG 551
|||||

QY 1008 TTCAGAAAAATGTTCTATGTCAGAGACAGACAGC-AGATCAGTGCACATCA 1062
|||||
Db 552 TTCAGAAAAATGTTCTATGTCAGAGACAGACAGAGAGAGATCAATGACATCA 607
|||||

RESULT 9
AA872079/c
LOCUS
DEFINITION
AA872079 602 bp mRNA EST 17-MAR-1998
O112407.s1 NCI-CGAP GC4 Homo sapiens cDNA clone IMAGE:1476276 3'
similar to TR:000180 O00180 P0RASSIUM CHANNEL KCNO1.; mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 602)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdip/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 78.
Location/Qualifiers
1. 602
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1476276"
/clone_lib="NCI-CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTZ19-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I and Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTZ19
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 159 a 137 c 124 g 182 t
ORIGIN

Query Match 25.2%; Score 477; DB 13; Length 602;
Best Local Similarity 90.9%; Pred. No. 9.2e-95;
Matches 552; Conservative 0; Mismatches 50; Indels 5; Gaps 4;

QY 978 ACCTTCTGTAATCCATGAGCTGAAAAATTCAGAAAAATGTTCTATGGAAGAAGAC 1037
|||||
Db 602 ACCCTGTGTGACATCATATGCT-AAAAATGAGATATG-TCTATGGAAG-ACGAC 547
|||||
QY 1038 AAGCAGAGATCAGTGCATCATATGACATGACCACTGCTCTCTCTGATCACA 1097
|||||
Db 546 GACGCGATATCATGAGTGCATCATATGACATGACCACTGCTCTCTCTGATCACA 487
|||||
QY 1098 GACGAGCAGCTGGCATGAAGAAGAGCAGAGCAAAATGAGCTTTGTGGCACCACG 1157
|||||
Db 486 GACGAGCAGCTGGCATGAAGAAGAGCAGAGCAAAATGAGCTTTGTGGCACCACG 427
|||||

	<i>/tissue_type="neoplastic oligodendroglioma"</i>							
	<i>/lab_host-DH10B</i>							
	<i>/note--Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGCGGAGGGCCGCAGTAGGTATTTCCTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."</i>							
BASE COUNT	122 a	117 c	92 g	144 t				
ORIGIN								
Query Match	Best Local Similarity	25.0%; Score 474;	DB 27;	Length 475;				
Matches 474;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
Db	864 CTGGGGGATTATGTGCCGTGGGAAAGGCTAACATAAATAATTCAGAGAGCTCATTAAGATT	923						
Db	475 CTGGGGGATTATGTSCCTGGGGGAAGGCTACATCAAAAATTCAGAGAGCTCATTAAGATT	416						
QY	924 GGGATCAGCTGTACTCTCTACTTTGGCCTTATTTGCCATGTTGTGATGTTCTGGAAACCCTTC	983						
Db	415 GGGATCACGTGTACTCTCTACTTTGGCCTTATTTGCCATGTTGTGATGTTCTGGAAACCCTTC	356						
QY	984 TGTGACATCCATGAGCTGAAAAAATTCAAGAAAAATGTTCTATGTAGAAGACAAGAC	1043						
Db	355 TGTGACATCCATGAGCTGAAAAAATTCAAGAAAAATGTTCTATGTAGAAGACAAGAC	296						
QY	1044 GAGGATCAGGTCACATCATAGAGCATGACCAACTGTCTTCCTCCATCGATCCAGACCG	1103						
Db	295 GAGGATCAGGTCACATCATAGAGCATGACCAACTGTCTTCCTCCATCGATCCAGACCG	236						
QY	1104 GCAGTGGCATGAAGAAGAGCACAAGCAAATGAGCCTTTGTGCCCCACCATCATCT	1163						
Db	235 GCAGTGGCATGAAGAAGAGCACAAGCAAATGAGCCTTTGTGCCCCACCATCATCT	176						
QY	1164 GCCTCGTGGATGAGGCCCTGCAAAACCATTTGAGGCGTATGTTGTCATTAATGCTAGAGCA	1223						
Db	175 GCCTCGTGGATGAGGCCCTGCAAAACCATTTGAGGCGTATGTTGTCATTAATGCTAGAGCA	116						
QY	1224 CCAGGTCAGGGTCGAAGAGAGGCTTAAGTATGTTCAATTTTATTCAGAAATGCAAAAGC	1283						
Db	115 CCAGGTCAGGGTCGAAGAGAGGCTTAAGTATGTTCAATTTTATTCAGAAATGCAAAAGC	56						
QY	1284 GAATAATTATGTCATTTAAGAAATAGCTACGTGTTGCAATGTCTTAATTAATAA	1337						
Db	55 GAATAATTATGTCATTTAAGAAATAGCTACGTGTTGCAATGTCTTAATTAATAA	2						
RESULT 11								
A1924793/c								
LOCUS	A1924793	484 bp	mRNA	EST	07-MAR-2000			
DEFINITION	wm3a04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446254	3'						
ACCESSION	A1924793							
VERSION	A1924793.1	GI:5660757						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
Eukaryote:	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia:	Eutheria; Primates; Catarrhini; Homnidae; Homo.							
NCl-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.							
Tumor Gene Index	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).							
Unpublished	(1997)							
Contact:	Robert Strausberg, Ph.D.							
Tel:	(301) 496-1550							
Email:	Robert.Strausberg@nih.gov							
LitProcurement:	Christopher Moskalko, M.D., Ph.D., Michael R.							

Db 278 GCCGACGTGAGACATCTCTGGGCCGCGTCTGGAGGCCAACAATATGAGATGCGT 337
 Oy 458 GGTGACGAACGCTGCGGCACTGGAACCTGAGACTTCACTCCGGCTCTTCTGGCCAG 517
 Db 338 GGTGACGAACGCTGCGGCACTGGAACCTGAGACTTCACTCCGGCTCTTCTGGCCAG 397
 Oy 518 CACCGTCTCTCCACACAGGTTATGGCCACACCGCTCTGTCAGATGAGATGAGC 577
 Db 398 CACCGTCTCTCCACACAGGTTATGGCCACACCGCTCTGTCAGATGAGATGAGC 457
 Oy 578 CTCTGCAATCATCTACTCCGTCATTCGATTCCTTACCTCTGTTCTGACGGCTGT 637
 Db 458 CTCTGCAATCATCTACTCCGTCATTCGATTCCTTACCTCTGTTCTGACGGCTGT 517
 Oy 638 GGTCCAGGCAATCAGCGTCAGTCAGTCCCGCAG 670
 Db 518 GGTCCAGGCAATCAGCGTCAGTCAGTCCCGCAG 550

RESULT 13

BE309179

LOCUS BE309179 742 bp mRNA EST 13-JUL-2000
 DEFINITION 601095044F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489466 5',
 mRNA sequence.

ACCESSION BE309179

VERSION BE309179.1 GI:9166970

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 742)

AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8530 row: h column: 11

High quality sequence stop: 541.

Location/Qualifiers

1..742

/organism="Mus musculus"

/strain="C57/B6"

/db_xref="taxon:10090"

/clone="IMAGE:3489466"

/clone_1lb="NCI CGAP Mam5"

/tissue_type="tumor, gross tissue"

/dev_stage="7 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 144 a 217 c 202 g 179 t
 ORIGIN

Query Match 22.1%; Score 419; DB 106; Length 742;

Best Local Similarity 85.8%; Pred. No. 5.6e-12;

Matches 500; Conservative 0; Mismatches 80; Indels 3; Gaps 3;

Oy 455 GGTGCTCAGCAACGCTGCGGCAAC-TGGAATCGGACTTCACTCCGCTCTTCTG 513
 Db 1 GGTGCTCAGCAACGCTGCGGCAAC-TGGAATCGGACTTCACTCCGCTCTTCTG 60

Oy 514 CCAGACCGTGCCTCCACACAGGTTATGGCCACACCGCTTGTGAGATGAGTA 573
 Db 61 CCAGACCGTGCCTCCACACAGGTTATGGCCACACCGCTTGTGAGATGAGTA 120
 Oy 574 AGGCTTCTGCATCATCTCTCGTATGAGATTCCTTCACTCCGCTTCTGACGG 633
 Db 121 AAGCTTCTGCATCATCTCTCGTATGAGATTCCTTCACTCCGCTTCTGACGG 180
 Oy 634 CTGTGTCAGGCAATCAGCTGACAGTCCGCGAGCGCGCTCTTCACTTCCATCC 693
 Db 181 CCGTGTCCAGGCTGACAGCTGACAGTCCGCGAGCGCGCTCTTCACTTCCATCC 240
 Oy 694 GGTGGGGCTTTCACAGAGGTTGGGCGCATGCTCATCCGCTGCTTGGGTTGTGA 753
 Db 241 GGTGGGGCTTTCACAGAGGTTGGGCGCATGCTCATCCGCTGCTTGGGTTGTGA 300
 Oy 754 CTGTGTCAGTCTTCTTCATCCGCGCGCTGCTTCTGACGCTGAGAGTACTGA 813
 Db 301 CCGTGTCCAGGCTGACAGCTGACAGTCCGCGAGCGCGCTCTTCACTTCCATCC 360
 Oy 814 ACTTCCGGAATCCTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 873
 Db 361 ACTTCCGGAATCCTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 420
 Oy 874 ATGTGCTGGGGAAGCTCAATCAAAATTCAGAGAGCTCTTAAAGATTGGATACGT 933
 Db 421 ATGTGCTGGGGAAGCTCAATCAAAATTCAGAGAGCTCTTAAAGATTGGATACGT 479
 Oy 934 GTTACCTGCTACTTGGGCTTATTCATGCTGATGTTGTAAGCTTCTGTAACCTC 993
 Db 480 GTTACCTGCTACTTGGGCTTATTCATGCTGATGTTGTAAGCTTCTGTAACCTC 538
 Oy 994 ATGAGCTGAAAAAATTCAGAAAAATGTTCTATGTGAAGAAGA 1036
 Db 539 ACAGAGCTGAAAAAATTCAGAAAAATGTTCTATGTGAAGAAGA 581

RESULT 14

AA858126/c

LOCUS AA858126/c 434 bp mRNA EST 21-APR-1998
 DEFINITION 05f5h07.s1 NCI_CGAP C08 Homo sapiens cDNA clone IMAGE:1435261 3',
 similar to TR:000180 000180 POTASSIUM CHANNEL KCN01.1, mRNA
 sequence.

ACCESSION AA858126
 VERSION AA858126.1 GI:2946428
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 434)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/dbtrp/image/image.html

Insert Length: 1249 Std Error: 0.00

Seq primer: -40m13 fwd. Et from Amersham

High quality sequence stop: 392.

Location/Qualifiers

1..434

/organism="Homo sapiens"

FEATURES

source

Wed Feb 21 15:16:09 2001

us-09-481-990-1.rst

Page 13

Qy 1003 AAAA 1006
| | |
Db 421 AAAA 424

Search completed: February 14, 2001, 02:55:31
Job time: 31605 sec

THIS PAGE BLANK (USPTO)